

Northeastern CAT

SAC Crystallography Crosscut Review '07

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Cornell University



Steven E. Ealick Olga Boudker Richard A. Cerione Brian R. Crane Jianhua Fu Ailong Ke Min Lu Holger Sondermann Hao Wu

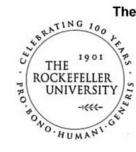
Harvard University



Stephen C. Harrison Daniel Kahne Lewis C. Cantley Bing Chen Jon Clardy Michael J. Eck Philip R. Dormitzer Barbara C. Furie Bruce Furie Rachelle Gaudet James M. Hogle David Jeruzalmi

Stephen C. Blacklow Robert E. Kingston Keith W. Miller Anjana Rao Tom Rapoport Steven E. Shoelson Piotr Sliz Timothy A. Springer Grea L. Verdine Suzanne Walker Jia-huai Wang

The Rockefeller University



Seth A. Darst **Gunter Blobel** Roderick MacKinnon **Charles Rice** Thomas P. Sakmar C. Erec Stebbins

Yale University



Thomas A. Steitz Joao M. Cabral Pietro De Camilli Ya Ha Elias Lolis Yorgo Modis Peter B. Moore Thomas D. Pollard Anne Marie Pyle Karin M. Reinisch Scott Strobel Yufeng Zhou Yong Xiong



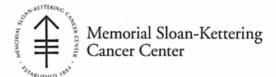
Massachusetts Institute of Technology

> Rober Sauer Tania A. Baker **David Bartel** Cartherine L. Drennan Robert Grant Barbara Imperialli Amy Keating Stephen J. Lippard Paul Matsudaira Alexander Rich Thomas Schwartz JoAnne Stubbe Michael B. Yaffe



Wayne A. Hendrickson Qing R. Fan John F. Hunt

Lawrence Shapiro Liang Tong Ming Zhou



Nikola Payletich Johnathan Goldberg Christopher D. Lima

Dimitar Nikolov Dinshaw Patel



Mission Statement:

Design, construct and operate synchrotron beamlines for technically challenging problems in structural biology using the APS Tandem Offset Undulator (TOU) and a standard sector dipole source.

Microdiffraction Hardware and Software for Tough Cases

Funded through a combination of Funds from our member institutions and a major grant from the NIH's National Center for Research Resources (P41).

50% share of Operational days to Institutional Members 50% share to our NCRR collaborators and APS General Users

Classes of Challenging Samples

Microscopic Crystals

Weak Diffractors

Large Unit Cells

Viruses - Steve Harrison: Herpes, Rotovirus,

Multisubunit complexes Molecular Machines with little internal symmetry

Jamie Cate: 70S ribosome

Tom Steitz 50S ribosome, DNA synthetases

Large Scale Projects

Cases requiring large scale screening

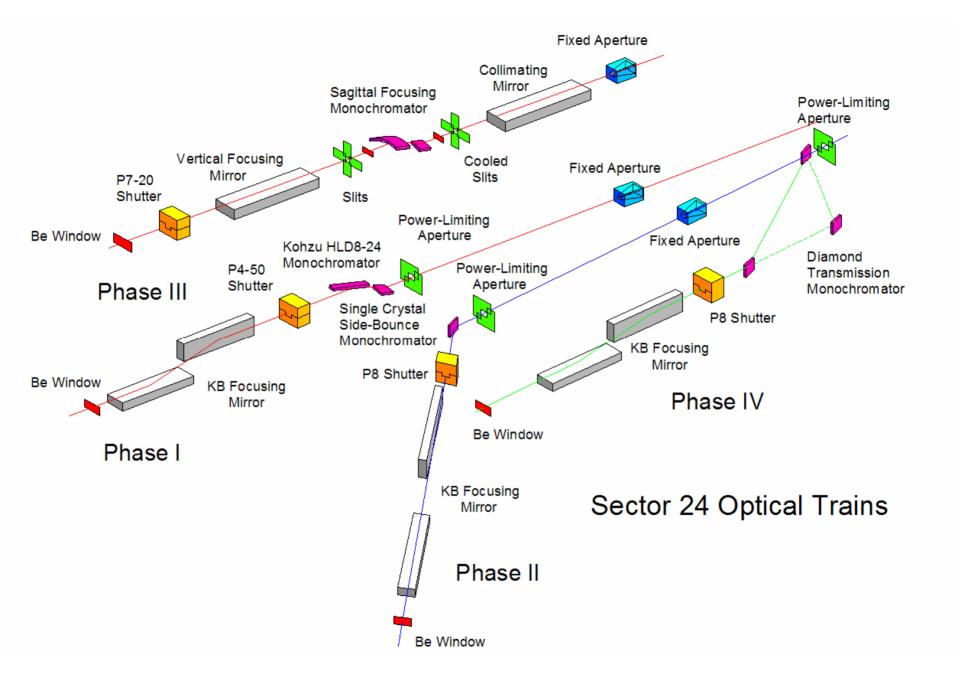
Tom Schwartz, Gunter Blobel: nuclear pore complex

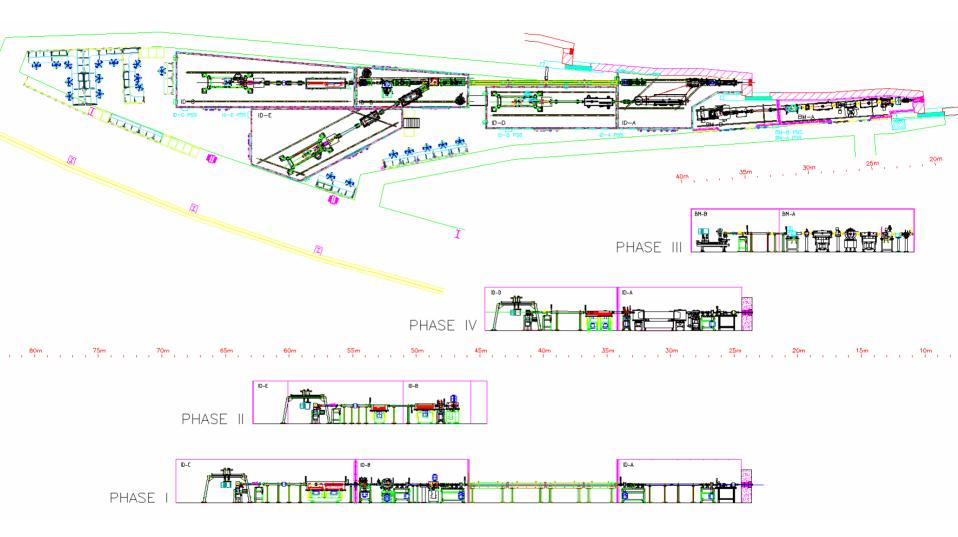
Nikola Pavletich: Kinases

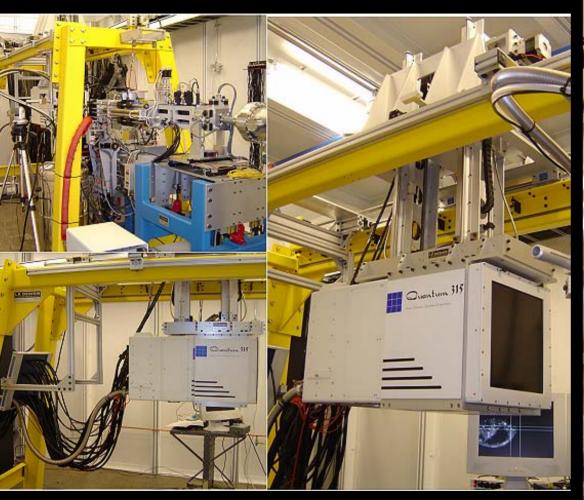
Functional Studies of Complex Molecular Machines - ribosomes

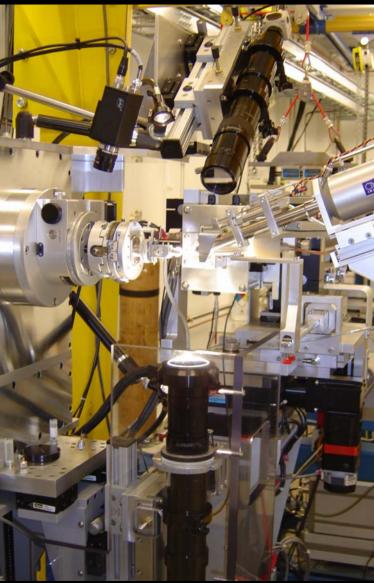
Longitudinal Studies, e.g. Pathways/Functional Networks

Steve Ealick: Nucleotide Metabolism









NE-CAT is specifically organized to address "challenging" data issues

1st Organizational principal is doctrinal:

NE-CAT beam lines are considered by staff and users to be reconfigurable, adaptable systems – even to the extent that this policy interferes with conventional productivity measures.

Hardware and Sofware issues

NE-CAT users are expected to collaborate with NECAT staff to define and evolve operational and technical range/scope of beam lines.

2nd Organizational principal: scale

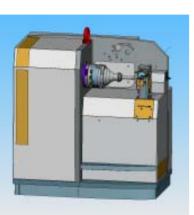
NE-CAT must have sufficient fiscal and manpower resources to evolve and adapt Sector 24 beam lines in response to changing user requirements

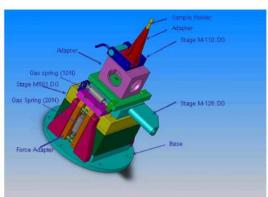
NE-CAT will have 4 beam lines with disparate operational envelopes.

- a) Therefore NE-CAT can realistically contemplate evolution (continuous development) of beam lines without incapacitating the entire operation.
- b) Once all beam lines are operational 24-ID-C can be evolved to satisfy changing user requirements.
- c) "Standard" or less demanding studies go to one of the other 3 beam lines.

Ongoing / Future Beam Line Developments

Microdiffraction – Support for micro crystals





Integration of MD2 microdiffractometer with 24-ID-E

Upgrade of 24-ID-C to microdiffraction capability

Logistical improvements – Support for all problem classes

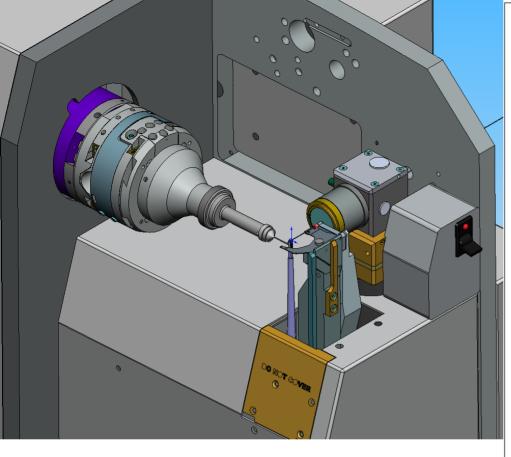
Robotic sample loader

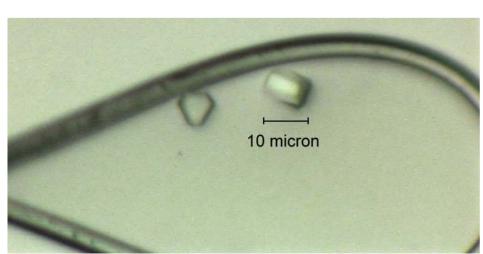
- reduce number of hutch entries
- 3.0 period undulators
 - avoid 1st to 3rd harmonic transistions

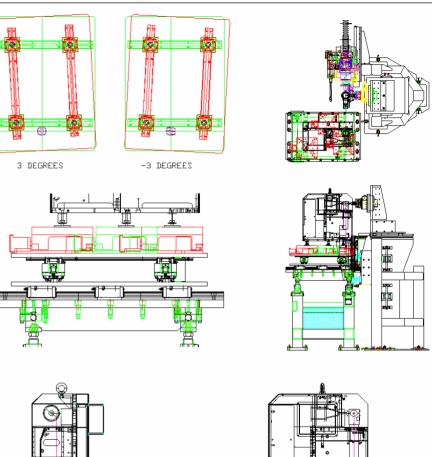
Clustered Computational Resource

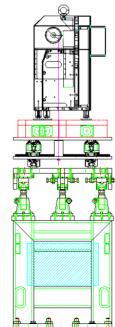
Telepresence for improved collaboration

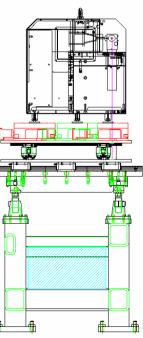






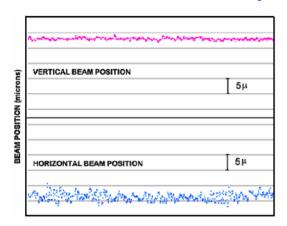






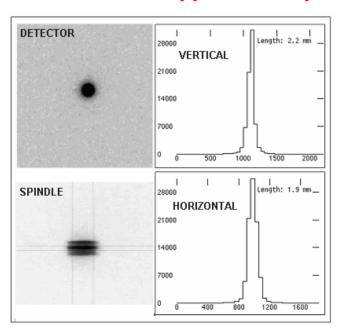
Ongoing / Future Beam Line Developments

Beam Positional Stability – Support for all problem classes



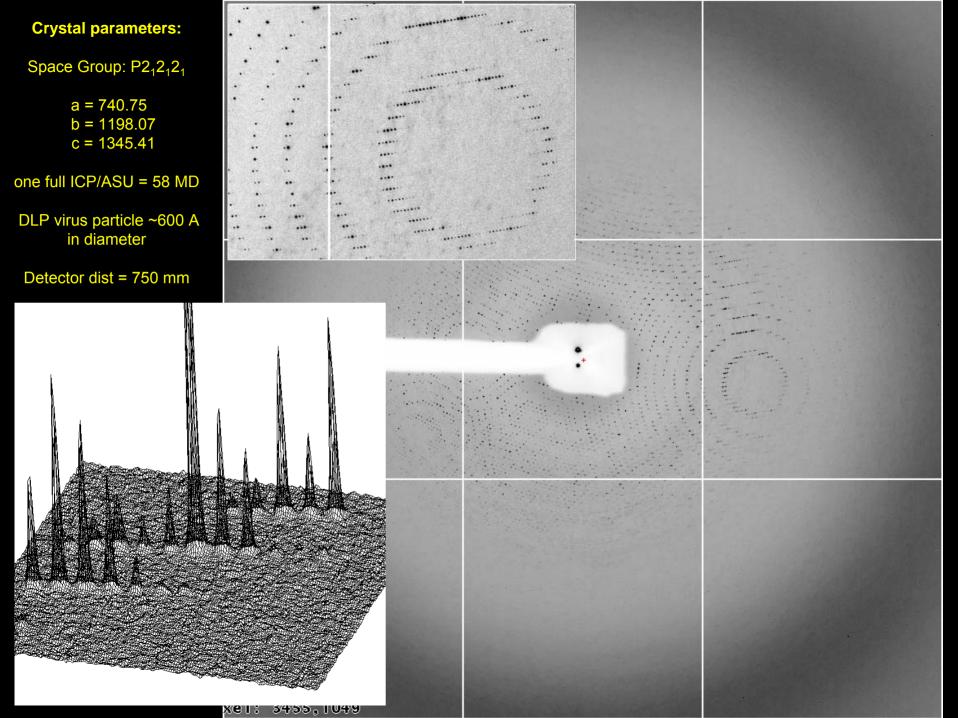
Elimination of residual flow-induced vibrations
Long baseline white BPM's to improve stability of
white beams
Improve mirror steering

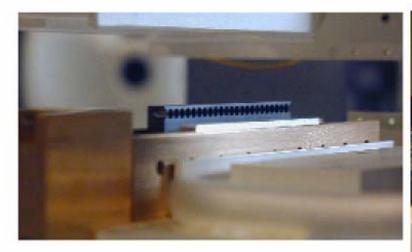
Beam Focus – Support for all problem classes



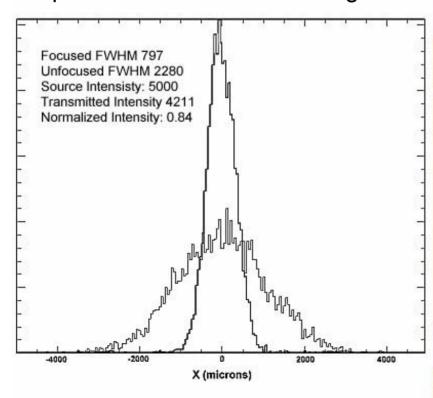
Compound Refractive Collimator
Increase Flux density
Reduce Horizontal Focus without
Increasing demagnification
Reduce horizontal divergence without
sacrificing focus
24-ID-C VFM converted to bimorph
Improved beam uniformity for
over/under-focused setups







Compound Refractive Collimating Lens





User Program / Productivity

Internal user program initiated mid 2005

Number of scientists visiting 24ID-C during 2006: 171

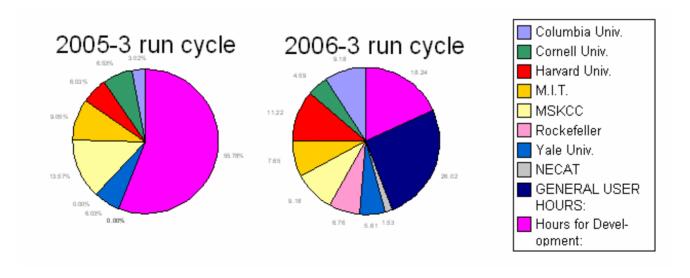
PDB submissions since late 2005: 57

Publications during 2006: 35

Cell: 3 Science: 3 Nature: 1 NSMB: 4 Mol Cell: 2 PNAS: 2

24ID-C entered APS GUP in 2006-3 run cycle

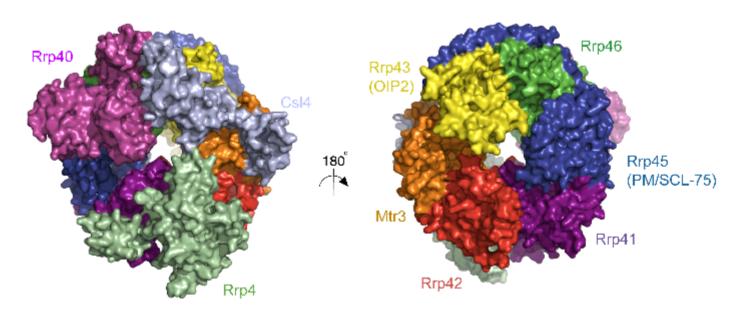
24ID-C User statistics



Science Highlights

Crystal Structure of the Eukaryotic RNA Exosome at 3.35Å Q. Liu, J.C. Greimann and C.D. Lima, Cell, 127, 2006, 1223-1237

- Degradation and processing of cellular RNA (rRNA, snoRNA, snRNA)
- •A 286kDa Reconstituted complex of nine proteins
- •Cubic space group with cell edge of 308Å
- •Radiation sensitive, hence a de-focussed beam was used to illuminate the whole ~200µ sized crystals

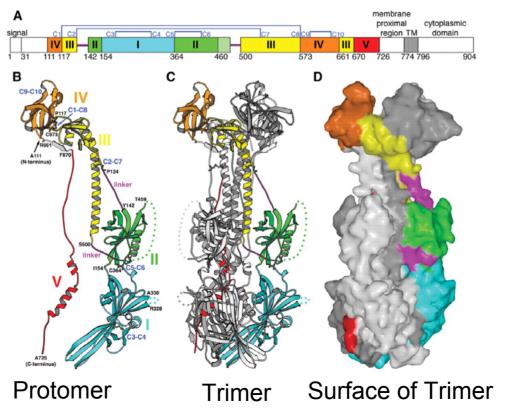


Two views of RNA Exosome

Science Highlights

Crystal Structure of Glycoprotein B from Herpes Simplex Virus 1 at 2.1Å E.E. Heldwein, H. Lou, F.C. Bender, G.H. Cohen, R.J. Eisenberg, S.C. Harrison, Science, 313, 2006, 217 - 220

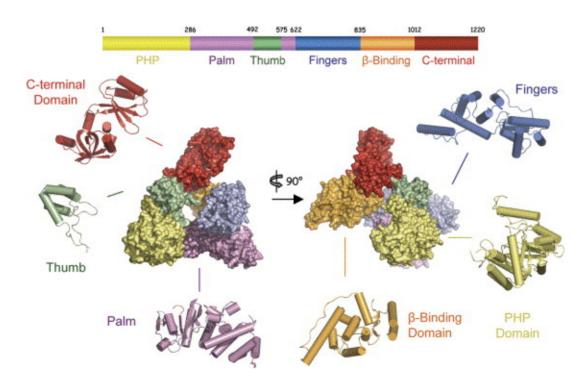
- •Part of Herpes Simplex Virus cell entry complex.
- •A trimer containing 1881 a.a. residues in total.
- •Spike dimensions: 85 x 80 x 160 Å.



Science Highlights

The Structure of *Thermus aquaticus* DNA Polymerase III at 3.0Å S. Bailey, R. A. Wing and T.A. Steitz, Cell, 126, 2006, 893-904

- •First eubacterial replicative DNA polymerase structure
- •A monomer of ~140kDa made-up of six domains
- •C222₁, *a*=175.1, *b*=186.9 and *c*=125.8Å



Taq DNA Polymerase III α subunit